Alpha Virus nsp1 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp1    MAAK--VHVDIEADSPFIKSLQKAFPSFEVESLQVTPNDHANARAFSHLATKLIEQETDK 58
RRV_nsp1    --MK--VTVDVEADSPFLKALQKAFPAFEVESQQVTPNDHANARAFSHLATKLIEQEVPA 56
ONV_nsp1    -MDS--VYVDIDADSAFLKALQQAYPMFEVEPKQVTPNDHANARAFSHLAIKLIEQEIDP 57
VEEV_nsp1   -MEK--VHVDIEEDSPFLRALQRSFPQFEVEAKQVTDNDHANARAFSHLASKLIETEVDP 57
SinV_nsp1   -MEKPVVNVDVDPQSPFVVQLQKSFPQFEVVAQQVTPNDHANARAFSHLASKLIELEVPT 59
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SFV_nsp1    DTLILDIGSAPSRRMMSTHKYHCVCPMRSAEDPERLDSYAKKLAAASGKVLDREIAGKIT 118
RRV_nsp1    NITILDVGSAPARRLMSDHSYHCICPMKSAEDPERLANYARKLAKTAGEVLDKNVSGKIT 116
ONV_nsp1    DSTILDIGSAPARRMMSDRKYHCVCPMRSAEDPERLANYARKLASAAGKVTDKNISGKIN 117
VEEV_nsp1   SDTILDIGSAPARRMYSKHKYHCICPMRCAEDPDRLYKYATKLKKNCKEITDKELDKKMK 117
SinV_nsp1   TATILDIGSAPARRMFSEHQYHCVCPMRSPEDPDRMMKYASKLAEKACKITNKNLHEKIK 119
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SFV_nsp1    DLQTVMATPDAESPTFCLHTDVTCRTAAEVAVYQDVYAVHAPTSLYHQAMKGVRTAYWIG 178
RRV_nsp1    DLQDVMATPDLESPTFCLHTDETCRTRAEVAVYQD---VHAPTSLYHQAMKGVRTVYWIG 173
ONV_nsp1    DLQAVMAVPNMETSTFCLHTDATCKQRGDVAIYQDVYAVHAPTSLYHQAIKGVRVAYWIG 177
VEEV_nsp1   ELAAVMSDPDLETETMCLHDDESCRYEGQVAVYQDVYAVDGPTSLYHQANKGVRVAYWIG 177
SinV_nsp1   DLRTVLDTPDAETPSLCFHNDVTCNMRAEYSVMQDVY-INAPGTIYHQAMKGVRTLYWIG 178
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SFV_nsp1    FDTTPFMFDALAGAYPTYATNWADEQVLQARNIGLCAASLTEGRLGKLSILRKKQLKPCD 238
RRV_nsp1    FDTTPFMFEVVAGAYPTYSTNWADEQVLQARNIGLCATSLSEGHRGKISIMRKKRLRPSD 233
ONV_nsp1    FDTTPFMYNAMAGAYPSYSTNWADEQVLKAKNIGLCSTDLSEGRRGKLSIMRGKKLKPCD 237
VEEV_nsp1   FDTTPFMFKNLAGAYPSYSTNWADETVLTARNIGLCSSDVMERSRRGMSILRKKYLKPSN 237
SinV_nsp1   FDTTQFMFSAMAGSYPAYNTNWADEKVLEARNIGLCSTKLSEGRTGKLSIMRKKELKPGS 238
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SFV_nsp1    TVMFSVGSTLYTESRKLLRSWHLPSVFHLKGKQSFTCRCDTIVSCEGYVVKKITMCPGLY 298
RRV_nsp1    -RMFSVG-TLYIESRRLLKSWHLPSVFHLKGKNSFTCRCDTIVSCEGYVVKKITMSPGTY 291
ONV_nsp1    RVLFSVGSTLYPESRKLLQSWHLPSVFHLKGKLSFTCRCDTIVSCEGYVVKRVTMSPGIY 297
VEEV_nsp1   NVLFSVGSTIYHEKRDLLRSWHLPSVFHLRGKQNYTCRCETIVSCDGYVVKRIAISPGLY 297
SinV_nsp1   RVYFSVGSTLYPEHRASLQSWHLPSVFHLNGKQSYTCRCDTVVSCEGYVVKKITISPGIT 298
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SFV_nsp1    GKTVGYAVTYHAEGFLVCKTTDTVKGERVSFPVCTYVPSTICDQMTGILATDVTPEDAQK 358
RRV_nsp1    GKTVGYAVTHHAEGFLMCKVTDTVRGERVSFPVCTYVPATICDQMTGILATDVTPEDAQK 351
ONV_nsp1    GKTSGYAVTHHAGGFLMCKTTDTVDGERVSFSVCTYVPATICDQMTGILATEVTPEDAQK 357
VEEV_nsp1   GKPSGYAATMHREGFLCCKVTDTLNGERVSFPVCTYVPATLCDQMTGILATDVSADDAQK 357
SinV_nsp1   GETVGYAVTHNSEGFLLCKVTDTVKGERVSFPVCTYIPATICDQMTGIMATDISPDDAQK 358
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SFV_nsp1    LLVGLNQRIVVNGRTQRNTNTMKNYLLPIVAVAFSKWAREYKADLDDEKPLGVRERSLTC 418
RRV_nsp1    LLVGLNQRIVVNGRTQRNTNTMKNYLLPVVAQAFSKWAREAKADMEDEKPLGTRERTLTC 411
ONV_nsp1    LLVGLNQRIVVNGRTQRNTNTMKNYLLPIVAQAFSKWAKECRKDMEDEKLLGVRERTLTC 417
VEEV_nsp1   LLVGLNQRIVVNGRTQRNTNTMKNYLLPVVAQAFARWAKEYKEDQEDERPLGLRDRQLVM 417
SinV_nsp1   LLVGLNQRIVINGRTNRNTNTMQNYLLPIIAQGFSKWAKERKDDLDNEKMLGTRERKLTY 418
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SFV_nsp1    CCLWAFKTRKMHTMYKKPDTQTIVKVPSEFNSFVIPSLWSTGLAIPVRSRIKMLLAKKTK 478
RRV_nsp1    CCLWAFKNHKTHTMYKRPDTQTIVKVPSTFDSFVIPSLWSSSLSIGIRQRIKLLLGPKLS 471
ONV_nsp1    CCLWAFRKHKTHTVYKRPDTQSIQKVPAEFDSFVIPSLWSSGLSIPLRTRIKWLLSKAPK 477
VEEV_nsp1   GCCWAFRRHKITSIYKRPDTQTIIKVNSDFHSFVLPRIGSNTLEIGLRTRIRKMLEEHKE 477
SinV_nsp1   GCLWAFRTKKVHSFYRPPGTQTCVKVPASFSAFPMSSVWTTSLPMSLRQKLKLALQPKKE 478
             * ***: :*   :.*: *.**: **   :* * :*  :. * :  :* ::: *      .

SFV_nsp1    -RELIPVLD-ASSARDAEQEEKERLEAELTREALPPLVPIAPAETG-VVDVDVEELEYHA 535
RRV_nsp1    -RDLPYSGD-RNEAREAEKEAEETKEAELTREALPPLVGSNCADD--VDQVDVEELTYRA 527
ONV_nsp1    YEQLPHSGN-AEEAAQAETDAVEEQEAELTREAMPPLQ--ATQDDI-QVEIDVEQLEDRA 533
VEEV_nsp1   PSPLITAED-IQEAKCAADEAKEVREAEELRAALPPLA--ADFEEP-TLEADVDLMLQEA 533
SinV_nsp1   EKLLQVSEELVMEAKAAFEDAQEEARAEKLREALPPLVADKGIEAAAEVVCEVEGLQADI 538
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SFV_nsp1      GA 537
RRV_nsp1      GA 529
ONV_nsp1      GA 535
VEEV_nsp1     GA 535
SinV_nsp1     GA 540
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